

Docket No. 1110-0307P

submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Substitute Sequence Listing, file "2002-12-06 1110-0307P.txt", is identical to the paper copy, except that it lacks formatting.

The amendment to the Specification is being made to replace the Sequence Listing as filed with the enclosed substitute Sequence Listing, which is compliant with the USPTO sequence requirements. No new matter is introduced by this amendment.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

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GMM/MAA/CVC
1110-0307P

Attachments: Disk Copy of Sequence Listing
 Paper Copy of Sequence Listing
 Copy of Notice to Comply

(Rev. 03/27/01)

<210> 2
 <211> 127
 <212> PRT
 <213> Mus sp.

<400> 2
 Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
 1 5 10 15
 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
 20 25 30
 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
 35 40 45
 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
 50 55 60
 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
 85 90 95
 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
 100 105 110
 Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

<210> 3
 <211> 408
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(408)

<400> 3
 atg gat tgg gtg tgg acc ttg cta ttc ctg ata gca gct gcc caa agt 48
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 1 5 10 15
 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30
 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 144
 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 aca gaa tat cca atg cac tgg gtg aag cag gct cca gga aag ggt ttc 192
 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 50 55 60
 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80

gaa gag ttc aag ggg cgg ttt gcc ttc tct ttg gag acc tct gcc agc 288
 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

act gcc tat ttg cag atc aac ttc ctc aaa aat gag gac acg gct aca 336
 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

tat ttc tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggc caa 384
 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125

ggc acc act ctc aca gtc tcc tca 408
 Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 4
 <211> 136
 <212> PRT
 <213> Mus sp.

<400> 4
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 1 5 10 15

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 50 55 60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125

Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 5
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(381)

<400> 5

atg	gag	acc	gat	acc	ctc	ctg	cta	tgg	gtc	ctc	ctg	cta	tgg	gtc	cca	48
Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	
1				5				10					15			
gga	tca	acc	gga	gat	att	cag	atg	acc	cag	agt	ccg	tcg	acc	ctc	tct	96
Gly	Ser	Thr	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	
			20					25					30			
gct	agc	gtc	ggg	gat	agg	gtc	acc	ata	act	tgc	agg	gca	agt	cag	gac	144
Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	
		35					40					45				
att	tcg	aat	tat	tta	aac	tgg	tat	cag	cag	aag	cca	ggc	aaa	gct	ccc	192
Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	
	50					55					60					
aag	ctt	cta	att	tat	tac	aca	tca	aga	tta	cac	tca	ggg	gta	cct	tca	240
Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	
65					70					75					80	
cgc	ttc	agt	ggc	agt	gga	tct	ggg	acc	aat	tat	acc	ctc	aca	atc	tcg	288
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asn	Tyr	Thr	Leu	Thr	Ile	Ser	
				85					90					95		
agt	ctg	cag	cca	gat	gat	ttc	gcc	act	tat	ttt	tgc	caa	cag	ggg	agt	336
Ser	Leu	Gln	Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Ser	
			100					105					110			
acg	ctt	ccg	tgg	acg	ttc	ggg	cag	ggg	acc	aag	gtg	gag	gtc	aaa		381
Thr	Leu	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys		
		115					120					125				

<210> 6
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 6

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5				10					15		
Gly	Ser	Thr	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser
			20					25					30		
Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp
		35					40					45			
Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
	50					55					60				
Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser
65					70					75					80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
115 120 125

<210> 7
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(408)

<400> 7

atg gat tgg gtg tgg acc ttg cta ttc ctg ata gct gca gcc caa agt	48
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser	
1 5 10 15	
gcc caa gca cag gtc cag ttg gtg cag tct gga gct gag gtg aag aag	96
Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct gga agc tca gtc aag gtg tcc tgc aaa gct tct ggg tat acc ttc	144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
aca gaa tat cca atg cac tgg gtg aga cag gct cca gga cag ggt ttc	192
Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe	
50 55 60	
aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct	240
Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala	
65 70 75 80	
gaa gag ttc aag gga cgg ttt aca ttc act ttg gac acc tct acc aac	288
Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn	
85 90 95	
act gcc tat atg gag ctc agc tct ctc agg tct gag gac acg gct gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggt caa	384
Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln	
115 120 125	
ggt acc ctg gtc aca gtc tcc tca	408
Gly Thr Leu Val Thr Val Ser Ser	
130 135	

<210> 8
<211> 136

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
50 55 60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
65 70 75 80

Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 9

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)..(1169)

<400> 9

ttttcttcca tttcaggtgt cgtgaggaat tcacc atg ctg ggc atc tgg acc 53
Met Leu Gly Ile Trp Thr
1 5

ctc cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
10 15 20

ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
25 30 35

agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
40 45 50

ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245

B1
cont

Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser
55 60 65 70

aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg 293
Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val
75 80 85

gaa ata aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca 341
Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro
90 95 100

aac ttt ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc 389
Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr
105 110 115

aaa tgt gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc 437
Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr
120 125 130

aag tgc aaa gag gaa gga tcc aga tct aac gag ccc aaa tct tgt gac 485
Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Glu Pro Lys Ser Cys Asp
135 140 145 150

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga 533
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
155 160 165

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc 581
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
170 175 180

tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa 629
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
185 190 195

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat 677
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
200 205 210

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt 725
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
215 220 225 230

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag 773
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
235 240 245

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag 821
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
250 255 260

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac 869
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
265 270 275

acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg 917
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
280 285 290

B1
Cont

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg	965
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
295 300 305 310	
gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg	1013
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
315 320 325	
ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac	1061
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	
330 335 340	
aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat	1109
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
345 350 355	
gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg	1157
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
360 365 370	
ggt aaa tga tag ggtaccttct gag	1182
Gly Lys	
375	

<210> 10
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala	
1 5 10 15	
Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys	
20 25 30	
Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly	
35 40 45	
Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp	
50 55 60	
Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu	
65 70 75 80	
Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr	
85 90 95	
Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu	
100 105 110	
His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys	
115 120 125	
Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn	
130 135 140	
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala	

ctg cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
 Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
 10 15 20

ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
 Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
 25 30 35

agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
 Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
 40 45 50

ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245
 Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser
 55 60 65 70

aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg 293
 Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val
 75 80 85

gaa ata aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca 341
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro
 90 95 100

aac ttt ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc 389
 Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr
 105 110 115

aaa tgt gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc 437
 Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr
 120 125 130

aag tgc aaa gag gaa gga tcc aga tct aac gag ccc aaa tct tgt gac 485
 Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Glu Pro Lys Ser Cys Asp
 135 140 145 150

aaa act cac aca tgc cca ccg tgc cca tag tga ggtaccttct gag 531
 Lys Thr His Thr Cys Pro Pro Cys Pro
 155

<210> 12
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15

Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys
 20 25 30

Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
 35 40 45

Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp
 50 55 60

Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu
65 70 75 80

Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr
85 90 95

Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu
100 105 110

His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys
115 120 125

Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
130 135 140

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
145 150 155
